

13 RE PCT/PTO 27 JUN 2002
10/069527

SEQUENCE LISTING

<110> The Horticulture and Food Research Institute of NZ

<120> Seedless Fruit Production

<130> 26329 MRB

<140>
<141>

<150> NZ337688
<151> 1999-09-07

<160> 7

<170> PatentIn Ver. 2.1

<210> 1

<211> 868

<212> DNA

<213> *Malus domestica*

<220>

<221> CDS

<222> (1)..(648)

<400> 1

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agg cag gtg acc tac tcc aag agg agg aat ggg att atc aag aag gca 96
Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Ile Lys Lys Ala
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aag gag atc act gtt cta tgt gat gct aaa gta tct ctt atc att tat 144
Lys Glu Ile Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Ile Tyr
      35           40           45

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tct agc tct ggg aag atg gtt gaa tac tgc agc cct tca act acg ctg 192
Ser Ser Ser Gly Lys Met Val Glu Tyr Cys Ser Pro Ser Thr Thr Leu
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aca gaa atc ttg gac aaa tac cat gga caa tct ggg aag aag ttg tgg 240
Thr Glu Ile Leu Asp Lys Tyr His Gly Gln Ser Gly Lys Lys Leu Trp
65          70          75          80

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gat gct aag cat gag aac ctc agc aat gaa gtg gat aga gtc aag aaa	288
Asp Ala Lys His Glu Asn Leu Ser Asn Glu Val Asp Arg Val Lys Lys	
85 90 95	

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gac aat gac agc atg caa gta gag ctc agg cat ctg aag gga gag gat 336
Asp Asn Asp Ser Met Gln Val Glu Leu Arg His Leu Lys Gly Glu Asp
          100      105      110

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atc aca tca ttg aac cat gta gag ctg atg gcc tta gag gaa gca ctt 384

Ile Thr Ser Leu Asn His Val Glu Leu Met Ala Leu Glu Glu Ala Leu
 115 120 125

gaa aat ggc ctt aca aat atc cgg gac aag cag tcc aag ttc gtc gac 432
 Glu Asn Gly Leu Thr Ser Ile Arg Asp Lys Gln Ser Lys Phe Val Asp
 130 135 140

atg atg aga gac aat gga aag gca ctg gaa gat gag aat aag cgc ctc 480
 Met Met Arg Asp Asn Gly Lys Ala Leu Glu Asp Glu Asn Lys Arg Leu
 145 150 155 160

act tat gag ctg caa aaa caa cag gag atg aaa ata aaa gag aat gtg 528
 Thr Tyr Glu Leu Gln Lys Gln Glu Met Lys Ile Lys Glu Asn Val
 165 170 175

aga aac atg gaa aat ggg tat cat cag agg cag ctg ggg aac tac aac 576
 Arg Asn Met Glu Asn Gly Tyr His Gln Arg Gln Leu Gly Asn Tyr Asn
 180 185 190

aac aac cag cag cag ata cct ttt gcc ttc cgc gtg cag cct att cag 624
 Asn Asn Gln Gln Gln Ile Pro Phe Ala Phe Arg Val Gln Pro Ile Gln
 195 200 205

cca aat ctc cag gag aga atc taa tttagatataat cttgcatttg catgctttt 678
 Pro Asn Leu Gln Glu Arg Ile
 210 215

cttaacttagt atatttatctc tccaccccttc tctctttttt catctgtcaa ggagttctta 738

agttttatgtc agatttccaa tggtttgtaa tggaaatttgc ttctgttatga ggctttgtt 798

tgaacccctgt aataattaag gctgtcatga actcggtttg tggaaaaaaa aaaaaaaaaa 858

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<210> 2
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 <213> Malus domestica

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 Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Ile Lys Lys Ala
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 Lys Glu Ile Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Ile Tyr
 35 40 45
 Ser Ser Ser Gly Lys Met Val Glu Tyr Cys Ser Pro Ser Thr Thr Leu
 50 55 60
 Thr Glu Ile Leu Asp Lys Tyr His Gly Gln Ser Gly Lys Lys Leu Trp
 65 70 75 80
 Asp Ala Lys His Glu Asn Leu Ser Asn Glu Val Asp Arg Val Lys Lys
 85 90 95
 Asp Asn Asp Ser Met Gln Val Glu Leu Arg His Leu Lys Gly Glu Asp
 100 105 110
 Ile Thr Ser Leu Asn His Val Glu Leu Met Ala Leu Glu Glu Ala Leu

115	120	125	
Glu Asn Gly Leu Thr Ser Ile Arg Asp Lys Gln Ser	Lys Phe Val Asp		
130	135	140	
Met Met Arg Asp Asn Gly Lys Ala Leu Glu Asp	Glu Asn Lys Arg Leu		
145	150	155	160
Thr Tyr Glu Leu Gln Lys Gln Gln Glu Met Lys	Ile Lys Glu Asn Val		
165	170	175	
Arg Asn Met Glu Asn Gly Tyr His Gln Arg Gln	Leu Gly Asn Tyr Asn		
180	185	190	
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Pro Asn Leu Gln Glu Arg Ile			
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<220>
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1	5	10	15
agg cag gtg acc tac tcc aag aga aat ggg atc ttc aag aag gct		96	
Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Phe Lys Ala			
20	25	30	
cag gag ctc acc gtt ctc tgt gat gcc aag gtc tcc ctc att atg ctc		144	
Gln Glu Leu Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Met Leu			
35	40	45	
tcc aac act aat aaa atg cac gag tat atc agc cct acc act acg acc		192	
Ser Asn Thr Asn Lys Met His Glu Tyr Ile Ser Pro Thr Thr Thr Thr			
50	55	60	
aag agt atg tat gat gac tat cag aaa act atg ggg atc gat ctg tgg		240	
Lys Ser Met Tyr Asp Asp Tyr Gln Lys Thr Met Gly Ile Asp Leu Trp			
65	70	75	80
agg aca cac gag gag tcg atg aaa gac acc ttg tgg aag ttg aaa gag		288	
Arg Thr His Glu Glu Ser Met Lys Asp Thr Leu Trp Lys Leu Lys Glu			
85	90	95	
atc aac aat aag ctg agg aga gag atc agg gag agg ttg ggc cat gat		336	
Ile Asn Asn Lys Leu Arg Arg Glu Ile Arg Gln Arg Leu Gly His Asp			
100	105	110	
cta aat ggc ctg agc ttt gac gag ctg gct tct ctt gac gat gag atg		384	
Leu Asn Gly Leu Ser Phe Asp Glu Leu Ala Ser Leu Asp Asp Glu Met			
115	120	125	

cag tct tcc ttg gat gcc ata cgt caa agg aag tac cat gtg atc aaa	432
Gln Ser Ser Leu Asp Ala Ile Arg Gln Arg Lys Tyr His Val Ile Lys	
130 135 140	
act cag acg gag acc acc aag aag gtt aag aac ttg gag caa aga	480
Thr Gln Thr Glu Thr Lys Lys Lys Val Lys Asn Leu Glu Gln Arg	
145 150 155 160	
aga gga aac atg ctg cat ggc tat ttt gac cag gaa gca gcc ggc gag	528
Arg Gly Asn Met Leu His Gly Tyr Phe Asp Gln Glu Ala Ala Gly Glu	
165 170 175	
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Asp Pro Gln Tyr Gly Tyr Glu Asp Asn Glu Gly Asp Tyr Glu Ser Ala	
180 185 190	
ctt gca ttg tca aat ggg gcg aat aac ttg tac act ttc cac ctc cac	624
Leu Ala Leu Ser Asn Gly Ala Asn Asn Leu Tyr Thr Phe His Leu His	
195 200 205	
cac cct aac ctc cac cac gga gga agc tcg ctc ggc tcc tcc att act	672
His Pro Asn Leu His His Gly Gly Ser Ser Leu Gly Ser Ser Ile Thr	
210 215 220	
cat ctg cac gat ctc cgc ctt gct tga tcgtgatctg agatatgatt	719
His Leu His Asp Leu Arg Leu Ala	
225 230	
aatcatcaact aagttatata ttaaggtcac ttataactgc ttttgctcta aagtgtttgc	779
ttggtgacta tctttagcga aggagttaga ctggactac ctctgaaaac agatgcataa	839
atatgtgtgt ggtgtttta tcaatgtatag cactaaaaaa atccgcgcgc ttgtgttttg	899
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Arg Gln Val Thr Tyr Ser Lys Arg Arg Asn Gly Ile Phe Lys Lys Ala	
20 25 30	
Gln Glu Leu Thr Val Leu Cys Asp Ala Lys Val Ser Leu Ile Met Leu	
35 40 45	
Ser Asn Thr Asn Lys Met His Glu Tyr Ile Ser Pro Thr Thr Thr	
50 55 60	
Lys Ser Met Tyr Asp Asp Tyr Gln Lys Thr Met Gly Ile Asp Leu Trp	
65 70 75 80	
Arg Thr His Glu Glu Ser Met Lys Asp Thr Leu Trp Lys Leu Lys Glu	

85	90	95	
Ile Asn Asn Lys Leu Arg Arg Glu	Ile Arg Gln Arg Leu Gly His Asp		
100	105	110	
Leu Asn Gly Leu Ser Phe Asp Glu	Leu Ala Ser Leu Asp Asp Glu Met		
115	120	125	
Gln Ser Ser Leu Asp Ala Ile Arg Gln Arg Lys Tyr His Val Ile Lys			
130	135	140	
Thr Gln Thr Glu Thr Thr Lys Lys Val	Lys Asn Leu Glu Gln Arg		
145	150	155	160
Arg Gly Asn Met Leu His Gly Tyr Phe Asp Gln Glu Ala Ala Gly Glu			
165	170	175	
Asp Pro Gln Tyr Gly Tyr Glu Asp Asn Glu Gly Asp Tyr Glu Ser Ala			
180	185	190	
Leu Ala Leu Ser Asn Gly Ala Asn Asn Leu Tyr Thr Phe His Leu His			
195	200	205	
His Pro Asn Leu His His Gly Gly Ser Ser Leu Gly Ser Ser Ile Thr			
210	215	220	
His Leu His Asp Leu Arg Leu Ala			
225	230		

<210> 5
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<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Made in lab

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<222> (14)
<223> n represents a, c, g, or t.

<220>
<221> allele
<222> (17)
<223> n represents a, c, g, or t.

<220>
<221> allele
<222> (20)
<223> n represents a, c, g, or t.

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25

<210> 6
<211> 30
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<220>
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<221> allele
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<223> n represents a, c, g, or t.

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<221> allele
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<223> n represents a, c, g, or t.

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30

<210> 7
<211> 20
<212> DNA
<213> Artificial Sequence

<220>
<223> Description of Artificial Sequence: Made in lab

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gagagagaac tagtctcgag

20